HERITABILITY AND REPEATABILITY OF METHANE EMISSIONS AND FEED INTAKE IN YOUNG DAIRY SIRES

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SUMMARY

Methane is a by-product of digestion in ruminants and is an important greenhouse gas linked to global warming. There is considerable interest in reducing methane emissions from ruminants. One method is through selection of sires with low methane emissions in their offspring. This research aimed to characterise genetic variation in methane emissions and dry matter intake (DMI) in growing dairy bulls identified from genomic prediction as genomic sires or participants in progeny testing schemes. Estimates of heritability and repeatability for methane emissions and DMI were low to moderate. Genetic and phenotypic correlations between methane emissions and DMI were positive, suggesting selection for reduced methane emissions would be associated with reduced DMI. After accounting for genetic variation in DMI, there was 77% of the genetic variation in methane emissions remaining, indicating there is scope to reduce daily methane emissions while maintaining DMI.

INTRODUCTION

Methane gas is generated as a by-product of digestion in ruminants and is one of the important greenhouse gases that have been linked with global warming (Herrero *et al.* 2016). There are global research efforts to reduce methane emissions from ruminants, especially dairy cattle (Herrero *et al.* 2016), one such method is through selection. Given that genetic progress is permanent and cumulative, it is an attractive option to reduce methane emissions. Methane emissions and dry matter intake (DMI) in ruminants have been reported to be positively phenotypically correlated (Breider *et al.* 2018; Herd *et al.* 2014), and genetically correlated (Manzanilla-Pech *et al.* 2021). Breeding dairy cattle for lower methane emissions may have an unfavourable impact on production and profitability through a correlated reduction in DMI. Measuring either methane or DMI is expensive and logistically challenging, especially in lactating dairy cattle, but unlike milk production traits can be measured in sire candidates.

The long-term goal of this project is to breed dairy cattle who produce less methane per kg DMI. This phase of the research aimed to characterise genetic variation in methane emissions and DMI in the dairy population using growing dairy bulls identified from genomic selection as genomic sires or participants in progeny testing schemes. Additionally, a genetic residual methane emissions trait was calculated using a restricted selection index (Kennedy *et al.* 1993) to assess the proportion of genetic variance in methane emissions that was genetically independent of DMI.

MATERIALS AND METHODS

Approval for animal experiments was granted by the AgResearch Animal Ethics Committee (#15176 and 15533). Experiments were conducted by LIC between February and June of each year (2021 and 2022) and by CRV between July and December 2021. Both farms were located in Waikato, New Zealand. Bulls were housed for 35 days, with the first 7-days as an acclimation period. The number of bulls per pen ranged from 5 to 12. Lucerne hay cubes (Multicube Stockfeeds,

Yarrawong, Vic) were fed in the week prior to the bulls entering the pens and then fed *ad lib.* in Hokofarm RIC2Discover Feed Intake (Hokofarm Group, Emmeloord, AX) bins, allowing individual animal intakes to be recorded. Methane emissions were measured using Greenfeed systems (GF; C-Lock Inc, Rapid City, SD). Animals were allowed to visit a GF device up to 6 times in each 24-hour period. CRV Youngstock Blend (SealesWinslow Ltd, Morrinsville, Waikato) pellets were fed as the bait feed in the GF, with animals allowed up to 24 drops of around 40g/drop in each 24-hour period.

Data handling. To obtain one daily methane "yield equivalent" value per bull, all visits within a day were summed to obtain the total methane and total time in seconds a bull was measured for methane. The calculation was as follows:

$$daily\ methane = \frac{\sum methane\ per\ visit}{\sum time\ (sec)\ at\ GF} * sec\ in\ a\ day$$

Daily DMI was calculated as the sum of the daily lucerne intake measured from the feed intake bins plus the concentrate intakes measured by the GF device.

After daily methane emissions and DMI data from the acclimation week were discarded, there were 13,109 daily methane emissions phenotypes and 12,687 daily DMI phenotypes from 486 bulls. Breeds represented were Jersey, Holstein, Friesian and crossbreeds of varying degrees.

Genotypes. The bulls included in the study were genotyped on a variety of SNP bovine panels. After applying a minor allele frequency filter of 0.1, there were 6,383 autosomal SNPs in common across panels for the 486 bulls.

Statistical analysis. A bivariate repeatability model was fitted using a Bayesian Monte Carlo Markov chain (MCMC) approach with the Julia for Whole-genome Analysis Software (JWAS v1.1.1) package (Cheng *et al.* 2018) run in a Julia computing environment (julialang.org). Inference was based on MCMC chains of 200,000 samples, retaining every 10th sample, after a burn-in of 25,000 samples which had been discarded.

The model equations were:
$$methane = CG + Year + BullPerm + M\alpha + e$$
$$DMI = CG + Year + BullPerm + M\alpha + e$$
where *methane* and *DMI* are the daily measurements on methane emissions (n=13,109 records on 474 bulls) and DMI (n=12,687 records on 485 bulls), respectively; CG was the fixed class effect of contemporary group of location-group-pen-day the bull was measured with; Year was the season-year the bull was measured in (2021 or 2022); BullPerm is the random permanent effect of bull assumed to be independently and identically normally distributed with variance σ_c^2; M is a matrix whose columns are additive dosage covariates for all of the 6,410 autosomal loci with effects independently and identically normally distributed with variance σ_a^2; α is a vector of the additive effects at each locus; and e is the residual effects independently and identically normally distributed with variance σ_e^2.

The 95% credibility intervals were calculated by taking the 97.5[th] percentiles of the MCMC samples (or functions of them that construct heritability or correlation samples from each sample of variance parameters) as the upper bounds and the 2.5[th] percentiles as the lower bounds.

Prior values for genetic, permanent environment and residual variances and covariances were based on dairy cattle literature (Berry and Crowley 2013; Breider *et al.* 2019; van Breukelen *et al.* 2022; Difford *et al.* 2020; Lassen *et al.* 2012; López-Paredes *et al.* 2020; Pickering *et al.* 2015).

RESULTS AND DISCUSSION
Estimates of heritability for daily methane emissions and daily DMI were low (Table 1). For methane emissions, this is on the lower end of estimates for heritability in dairy cattle of 0.12 to 0.45

(Breider *et al.* 2018, 2019; van Breukelen *et al.* 2022; Difford *et al.* 2020; López-Paredes *et al.* 2020). A study using sniffers reported that when recorded as a mean daily value the heritability of methane emissions was 0.13, similar to the 0.10 reported in the current study. Whereas heritability was higher at 0.32 if the records were averaged over a week due to a large decline in the residual variance when averaging records (van Breukelen *et al.* 2022). In young beef cattle the heritability of methane was reported as 0.27 based on 2 consecutive 24-hour periods in respiration chambers (Donoghue *et al.* 2016).

Similar to methane emissions, the estimate for the heritability of DMI was at the low end of the range previously reported in dairy cattle of 0.11 to 0.43 (Berry and Crowley 2013; Difford *et al.* 2020; Pickering *et al.* 2015).

Table 1. Phenotypic mean and standard deviation (SD) of daily methane emissions (g/d) and dry matter intake (DMI; kg/d) and posterior means (95% credibility intervals) for the genetic variance, heritability, repeatability and genetic and phenotypic correlations

Trait	Methane	DMI
Mean ± SD	229.7 ± 52.7	10.3 ± 3.0
Genetic variance	177 (101, 272)	0.39 (0.20, 0.65)
Heritability	0.10 (0.06, 0.15)	0.09 (0.05, 0.15)
Repeatability	0.31 (0.28, 0.34)	0.37 (0.33, 0.40)
Correlations		
Genetic	0.47 (0.15, 0.71)	
Phenotypic	0.28 (0.24, 0.31)	

Estimates of repeatability for both methane and DMI were moderate (Table 1) but lower than that reported elsewhere in dairy cattle (Breider *et al.* 2019; Difford *et al.* 2020; López-Paredes *et al.* 2020), with the exception of Lassen *et al.* (2012) and van Breukelen *et al.* (2022) who reported repeatabilities of 0.3 to 0.34 for daily methane emissions.

The phenotypic correlation between methane emissions and DMI was 0.28 and was in the range of 0.01 to 0.49 based on reports in lactating dairy cattle by others (Breider *et al.* 2018; Difford *et al.* 2018, 2020; Manzanilla-Pech *et al.* 2021). To our knowledge there are no literature estimates of the correlations between methane emissions and DMI in young growing dairy bulls. Studies in young beef cattle have reported phenotypic correlations between methane emissions and DMI of 0.65 (Herd *et al.* 2014) and 0.71 (Donoghue *et al.* 2016), higher than that reported in the current study. Both of those studies in beef cattle were conducted over 2 consecutive 24-hour periods using respiration chambers.

Based on studies in growing beef cattle, a positive genetic correlation between methane and DMI was expected in growing dairy bulls (Donoghue *et al.* 2016). The posterior mean of the genetic correlation between methane emissions and DMI in the current study was 0.47 with a 95% credibility interval of 0.15 to 0.71, similar to 0.42 reported by Manzanilla-Pech *et al.* (2021), based on 2,990 lactating dairy cattle and 0.42 reported by Richardson *et al.* (2021) based on 379 lactating dairy cattle. Difford *et al.* (2020) reported the genetic correlations between methane and DMI based on two populations of Holstein-Friesian cattle in either Denmark or The Netherlands. For the Danish population, they reported a genetic correlation of 0.6 but for the Dutch population the found the correlation to be -0.09 between the two traits (Difford *et al.* 2020). The authors postulated that the difference in estimates between the two populations studied may have been due to the influence of stage of lactation and differences in diet composition between the two countries (Difford *et al.* 2020).

After accounting for genetic variation in DMI by using partial genetic regression (Kennedy *et al.* 1993), the genetic variance of methane reduced from 177 $(g/d)^2$ to 136 $(g/d)^2$, which is 77% of

the genetic variation in methane remaining. The resulting heritability of methane after accounting for variation in DMI was 0.08 and the genetic correlation with DMI was zero, indicating there is scope to reduce daily methane emissions while maintaining DMI.

CONCLUSIONS

There is genetic variation in methane emissions and in DMI for growing dairy bulls. Additionally, there are positive genetic and phenotypic correlations between methane emissions and DMI, suggesting that selection to decrease methane emissions would lead to reduced DMI. Nevertheless, there is opportunity to reduce daily methane emissions from dairy bulls, whilst maintaining DMI due to a considerable proportion of the genetic variance in methane emissions being independent of DMI.

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